

SEQUENCE LISTING

<110> ALDAZ, MARCELO C.
BEDNAREK, ANDRZEJ

<120> WWOX: A PUTATIVE TUMOR SUPPRESSOR GENE MUTATED IN
MULTIPLE CANCERS

<130> UTSC:671US

<140> UNKNOWN

<141> 2001-10-15

<150> 60/240,277

<151> 2000-10-13

<160> 68

<170> PatentIn Ver. 2.1

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<212> PRT

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35 40 45

Thr Gly Lys Arg Lys Arg Val Ala Gly Asp Leu Pro Tyr Gly Trp Glu
50 55 60

Gln Glu Thr Asp Glu Asn Gly Gln Val Phe Phe Val Asp His Ile Asn
65 70 75 80

Lys Arg Thr Thr Tyr Leu Asp Pro Arg Leu Ala Phe Thr Val Asp Asp
85 90 95

Asn Pro Thr Lys Pro Thr Thr Arg Gln Arg Tyr Asp Gly Ser Thr Thr
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Val Thr Gly Ala Asn Ser Gly Ile Gly Phe Glu Thr Ala Lys Ser Phe
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Ala Ser Glu Ala Val Ser Arg Ile Leu Glu Glu Trp His Lys Ala Lys
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 Cys Asn Ala Ala Thr Phe Ala Leu Pro Trp Ser Leu Thr Lys Asp Gly
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 Ala Met Leu Ala Tyr Asn Arg Ser Lys Leu Cys Asn Ile Leu Phe Ser
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 Asn Glu Leu His Arg Arg Leu Ser Pro Arg Gly Val Thr Ser Asn Ala
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 tccacagtca gcc atg gca gcg ctg cgc tac gcg ggg ctg gac gac acg 169
 Met Ala Ala Leu Arg Tyr Ala Gly Leu Asp Asp Thr
 1 5 10

gac agt gag gac gag ctg cct ccg ggc tgg gag gag aga acc acc aag 217
 Asp Ser Glu Asp Glu Leu Pro Pro Gly Trp Glu Glu Arg Thr Thr Lys
 15 20 25

gac ggc tgg gtt tac tac gcc aat cac acc gag gag aag act cag tgg 265
 Asp Gly Trp Val Tyr Tyr Ala Asn His Thr Glu Glu Lys Thr Gln Trp
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gaa cat cca aaa act gga aaa aga aaa cga gtg gca gga gat ttg cca 313
 Glu His Pro Lys Thr Gly Lys Arg Lys Arg Val Ala Gly Asp Leu Pro
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tac gga tgg gaa caa gaa act gat gag aac gga caa gtg ttt ttt gtt 361
 Tyr Gly Trp Glu Gln Glu Thr Asp Glu Asn Gly Gln Val Phe Phe Val
 65 70 75

gac cat ata aat aaa aga acc acc tac ttg gac cca aga ctg gcg ttt 409
 Asp His Ile Asn Lys Arg Thr Thr Tyr Leu Asp Pro Arg Leu Ala Phe
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 Thr Val Asp Asp Asn Pro Thr Lys Pro Thr Arg Gln Arg Tyr Asp
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 Gly Ser Thr Thr Ala Met Glu Ile Leu Gln Gly Arg Asp Phe Thr Gly
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agg gat gta ctt caa caa ctg ctg ccg ctg cat gcc ctc acc aga agc		649	
Arg Asp Val Leu Gln Gln Leu Leu Pro Leu His Ala Leu Thr Arg Ser			
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Ser Glu Arg Arg Asp Gly Pro Asp Pro Val Gly Ala Gln Arg Glu Ala			
175	180	185	
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Asp Pro Arg Thr Ala Trp Gln Pro Val Arg Leu Ser Gly Ala Gln Ser			
190	195	200	
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Gly Trp Ala His Thr Pro Ala Leu Cys Val Ser Pro His Ala Ser Ala			
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Arg Ala Gly Pro Leu Pro Asn Val Pro Thr Gln Ile Arg Lys Ser			
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aaa gga aat aag agc agt cac aac aga gtg aaa aat ctt aag tac caa		889	
Lys Gly Asn Lys Ser Ser His Asn Arg Val Lys Asn Leu Lys Tyr Gln			
240	245	250	
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Trp Glu Ala Gly Asn Ser Trp Gly Lys Val Ser Leu Phe Trp Gly Trp			
255	260	265	
gct agg cat agg tct ctt tgc ttt ctg gtg gtg gcc tgt ttg aaa gta		985	
Ala Arg His Arg Ser Leu Cys Phe Leu Val Val Ala Cys Leu Lys Val			
270	275	280	
aaa acc tgc ttg gtg tgt agg ttc cgt atc tcc ctg gag aag cac cag		1033	
Lys Thr Cys Leu Val Cys Arg Phe Arg Ile Ser Leu Glu Lys His Gln			
285	290	295	300
caa ttc tct ttc ttt tac tgt tat aga ata gcc tga ggtccccctcg		1079	
Gln Phe Ser Phe Phe Tyr Cys Tyr Arg Ile Ala			
305	310		
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1625

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35 40 45
Thr Gly Lys Arg Lys Arg Val Ala Gly Asp Leu Pro Tyr Gly Trp Glu
50 55 60
Gln Glu Thr Asp Glu Asn Gly Gln Val Phe Phe Val Asp His Ile Asn
65 70 75 80
Lys Arg Thr Thr Tyr Leu Asp Pro Arg Leu Ala Phe Thr Val Asp Asp
85 90 95
Asn Pro Thr Lys Pro Thr Thr Arg Gln Arg Tyr Asp Gly Ser Thr Thr
100 105 110
Ala Met Glu Ile Leu Gln Gly Arg Asp Phe Thr Gly Lys Val Val Val
115 120 125
Val Thr Gly Ala Asn Ser Gly Ile Ala Thr Gly Ser Cys His His Arg
130 135 140
Val Leu Cys Cys Cys Pro Arg Thr Gly Gly Ser Gly Arg Asp Val Leu
145 150 155 160
Gln Gln Leu Leu Pro Leu His Ala Leu Thr Arg Ser Ser Glu Arg Arg
165 170 175
Asp Gly Pro Asp Pro Val Gly Ala Gln Arg Glu Ala Asp Pro Arg Thr
180 185 190
Ala Trp Gln Pro Val Arg Leu Ser Gly Ala Gln Ser Gly Trp Ala His
195 200 205
Thr Pro Ala Leu Cys Val Ser Pro His Ala Ser Ala Arg Ala Gly Pro
210 215 220
Leu Pro Asn Val Pro Pro Thr Gln Ile Arg Lys Ser Lys Gly Asn Lys
225 230 235 240
Ser Ser His Asn Arg Val Lys Asn Leu Lys Tyr Gln Trp Glu Ala Gly
245 250 255
Asn Ser Trp Gly Lys Val Ser Leu Phe Trp Gly Trp Ala Arg His Arg
260 265 270
Ser Leu Cys Phe Leu Val Val Ala Cys Leu Lys Val Lys Thr Cys Leu
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		Met	Ala	Ala	Leu	Arg	Tyr	Ala	Gly	Leu	Asp	Asp	Thr	
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 Asp Ser Glu Asp Glu Leu Pro Pro Gly Trp Glu Glu Arg Thr Thr Lys

15	20	25												
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30	35	40												
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45	50	55	60											
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 Tyr Gly Trp Glu Gln Glu Thr Asp Glu Asn Gly Gln Val Phe Phe Val

65	70	75												
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80	85	90												
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act gtg gat gat aat ccg acc aag cca acc acc cgg caa aga tac gac 457
 Thr Val Asp Asp Asn Pro Thr Lys Pro Thr Thr Arg Gln Arg Tyr Asp

95	100	105												
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ggc agc acc act gcc atg gaa att ctc cag ggc cgg gat ttc act ggc 505
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110	115	120												
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125	130	135	140											
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145	150	155												
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caa	cag	gga	gct	gcc	acc	acc	gtg	tac	tgt	gct	gct	gtc	cca	gaa	ctg	697	
Gln	Gln	Gly	Ala	Ala	Thr	Thr	Val	Tyr	Cys	Ala	Ala	Val	Pro	Glu	Leu		
175																185	
gag	ggt	ctg	gga	ggg	atg	tac	ttc	aac	aac	tgc	tgc	cgc	tgc	atg	ccc	745	
Glu	Gly	Leu	Gly	Gly	Met	Tyr	Phe	Asn	Asn	Cys	Cys	Arg	Cys	Met	Pro		
190																195	
tca	cca	gaa	gct	cag	agc	gaa	gag	acg	gcc	cg	acc	ctg	tgg	g	ctc	793	
Ser	Pro	Glu	Ala	Gln	Ser	Glu	Glu	Thr	Ala	Arg	Thr	Leu	Trp	Ala	Leu		
205																210	
agc	gag	agg	ctg	atc	caa	gaa	cgg	ctt	ggc	agc	cag	tcc	ggc	taa		838	
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35 40 45

Thr Gly Lys Arg Lys Arg Val Ala Gly Asp Leu Pro Tyr Gly Trp Glu
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Gln Glu Thr Asp Glu Asn Gly Gln Val Phe Phe Val Asp His Ile Asn
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Lys Arg Thr Thr Tyr Leu Asp Pro Arg Leu Ala Phe Thr Val Asp Asp
85 90 95

Asn Pro Thr Lys Pro Thr Thr Arg Gln Arg Tyr Asp Gly Ser Thr Thr
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Ala Met Glu Ile Leu Gln Gly Arg Asp Phe Thr Gly Lys Val Val Val
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Val Thr Gly Ala Asn Ser Gly Ile Gly Phe Glu Thr Ala Lys Ser Phe
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145 150 155 160

Ala Ser Glu Ala Val Ser Arg Ile Leu Glu Trp Gln Gln Gly Ala
165 170 175

Ala Thr Thr Val Tyr Cys Ala Ala Val Pro Glu Leu Glu Gly Leu Gly
180 185 190

Gly Met Tyr Phe Asn Asn Cys Cys Arg Cys Met Pro Ser Pro Glu Ala
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